

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 2, 2003, 12:39:57 ; Search time 21 Seconds
(without alignments)
2238.559 Million cell updates/sec

Title: US-09-455-978b-2

Perfect score: 2394
Sequence: 1 MSNDNDTLVTADVRNIDGH.....ATDQVRYVEVREYVGRKLS 489

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: PIR-73:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2394	100.0	489	2	T44978 transducer protein
2	2360	98.6	489	2	E84304 Htr10 transducer (
3	643	26.9	481	2	A84294 Htr9 transducer (1
4	609.5	25.5	482	2	T44973 transducer protein
5	597	24.9	633	2	H84336 Htr3 transducer (1
6	580	24.9	805	2	T48840 transducer protein
7	580	24.2	790	2	B84238 Htr18 transducer (1
8	578	24.1	778	2	F84237 Htr14 transducer (1
9	573	23.9	778	2	T48897 transducer protein
10	560.5	23.4	452	2	T48499 transducer protein
11	555	23.2	810	2	F84337 Htr5 transducer (1
12	554	23.1	810	2	T46870 halobacterial tran
13	540.5	22.6	777	2	T44537 transducer protein
14	537.5	22.5	534	2	S55299 sensory rhodopsin
15	535.5	22.4	636	2	A84252 Htr15 transducer (1
16	529	22.1	804	2	T44964 transducer protein
17	524	21.9	451	2	T44964 transducer protein
18	523.5	21.9	544	2	T44938 transducer protein
19	523.5	21.9	643	2	H84305 Htr8 transducer (1
20	521.5	21.8	628	2	F84219 Htr16 transducer (1
21	521	21.8	545	2	E84327 Htr7 transducer (1
22	521	21.8	545	2	T46811 halobacterial tran
23	509.5	21.3	789	2	E84236 transducer protein
24	507.5	21.2	788	2	T44252 transducer protein
25	506	21.1	420	2	C84238 Htr12 transducer (1
26	505	21.1	642	1	T44253 transducer protein
27	502.5	21.0	773	2	T44989 Htr14 transducer (1
28	499.5	20.9	627	2	F84194 transducer protein
29	497.5	20.8	419	2	T44276 transducer protein

30	497	20.8	536	2	D84325 Htr17 transducer (
31	475.5	19.9	537	2	C87302 methyl-accepting c
32	464	19.4	764	2	A84328 Htr2 transducer (1
33	463.5	19.4	536	1	A41190 transducer protein
34	463.5	19.4	536	2	E84318 Htr1 transducer (1
35	461	19.3	765	1	T44946 transducer protein
36	452.5	18.9	423	2	H84257 Htr3 transducer (1
37	439.5	18.4	423	2	T44258 transducer protein
38	419.5	17.5	559	2	G84132 methyl-accepting c
39	415	17.3	555	2	D87536 methyl-accepting c
40	413	17.3	439	2	A83713 methyl-accepting c
41	412.5	17.2	432	2	C69832 methyl-accepting c
42	409.5	17.1	632	2	H83106 chemotactic transd
43	408	17.0	499	2	A97485 methyl-accepting c
44	408	17.0	499	2	AB2703 methyl-accepting c
45	405.5	16.9	579	2	D84137 methyl-accepting c

ALIGNMENTS

RESULT 1

T44978 transducer protein hemAT [validated] - Halobacterium salinarum

N:Alternate names: methyl-accepting taxis protein htb; transducer protein htb; transd

C:Species: Halobacterium salinarum

C>Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 15-Sep-2000

C/Accession: T44978

R:Zhang, W.; Brooun, A.; McCandless, J.; Banda, P.; Alam, M.

Proc. Natl. Acad. Sci. U.S.A. 93, 4649-4654, 1996

A:Title: Signal transduction in the archaeon Halobacterium salinarum is processed

A:Reference number: 222804; PMID:96209786; PMID:8643458

A/Accession: T44978

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-489 <ZHA>

A/Cross-references: EMBL:U75436; NID:g1654420; PIDN:AAB17881.1; PID:g1654421

A:Experimental source: strain Flx15

A/Note: The source is designated as Halobacterium salinarum

C/Genetics:

A/Gene: hemAT; htp15; htb

C/Function:

A:Description: Involved in aerotactic signal transduction; Involved in oxygen sensing

C:Superfamily: Halobacterium salinarum transducer protein htr1

C:Keywords: heme; methylated amino acid; signal transduction

Query Match	100.0%	Score 2394;	DB 2;	Length 489;
Best Local Similarity	100.0%	Pred. No. 8	4e-98;	
Matches 489;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps
QY	1	MSNDNDTLVTADVRNIDGH	ADAEIAWRISFTGIDDDTYMAALAEQPLEAT	60
DB	1	MSNDNDTLVTADVRNIDGH	ADAEIAWRISFTGIDDDTYMAALAEQPLEAT	60
QY	61	ADALVTDFYHLESEYRTODLFANSTVTEQLKETOQEVYLLGGRGYDEYVAQRARIG	120	
DB	61	ADALVTDFYHLESEYRTODLFANSTVTEQLKETOQEVYLLGGRGYDEYVAQRARIG	120	
QY	121	KIHVDLGLGPDVYVYAGATRYTGLDALADVDVADREBEAAAVDELVAFLPMLKLTLE	180	
DB	121	KIHVDLGLGPDVYVYAGATRYTGLDALADVDVADREBEAAAVDELVAFLPMLKLTLE	180	
QY	181	DOQIAMDYIDSYAQRRLHDEIDSRQELANNAVHVEAPLSLEATSDVAREDTMART	240	
DB	181	DOQIAMDYIDSYAQRRLHDEIDSRQELANNAVHVEAPLSLEATSDVAREDTMART	240	
QY	241	DDQVDRADVSRREISSVSAVEEVAFTADVRRTSEEAALAOGEAADALATMTDID	300	
DB	241	DDQVDRADVSRREISSVSAVEEVAFTADVRRTSEEAALAOGEAADALATMTDID	300	
QY	301	EATDGVATAGVEQLGERADVESVGVTDIDIAEQTNMLALANSTEARAGGEGFAVAD	360	
DB	301	EATDGVATAGVEQLGERADVESVGVTDIDIAEQTNMLALANSTEARAGGEGFAVAD	360	